```
<!--StartFragment-->RESULT 6
AGLA_RHIME
ΙD
    AGLA RHIME
                            Reviewed:
                                        551 AA.
AC
    Q9Z3R8;
DT
    30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT
    02-NOV-2001, sequence version 2.
DT
    24-JUL-2007, entry version 44.
DE
    Probable alpha-glucosidase (EC 3.2.1.20).
GN
    Name=aqlA; OrderedLocusNames=R00698; ORFNames=SMc03064;
    Rhizobium meliloti (Sinorhizobium meliloti).
OS
OC
    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC
    Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX
    NCBI_TaxID=382;
RN
    [1]
RP
    NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX
    MEDLINE=99328961; PubMed=10400573;
RA
    Willis L.B., Walker G.C.;
    "A novel Sinorhizobium meliloti operon encodes an alpha-glucosidase
RT
RT
    and a periplasmic-binding-protein-dependent transport system for
RT
    alpha-glucosides.";
    J. Bacteriol. 181:4176-4184(1999).
RN
    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP
RC
    STRAIN=1021;
    MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RX
RA
    Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
    Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA
RA
    Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
    Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA
RA
    Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
    "Analysis of the chromosome sequence of the legume symbiont
RT
RT
    Sinorhizobium meliloti strain 1021.";
    Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
RL
CC
    -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
CC
        linked alpha-D-glucose residues with release of alpha-D-glucose.
CC
    -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC
     _____
CC
    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC
    Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR
    EMBL; AF045609; AAD12047.1; -; Genomic_DNA.
    EMBL; AL591784; CAC45270.1; -; Genomic_DNA.
DR
DR
    HSSP; P21332; 1UOK.
DR
    GenomeReviews; AL591688_GR; R00698.
    KEGG; sme:SMc03064; -.
    BioCyc; SMEL266834:SMC03064-MONOMER; -.
    GO; GO:0004558; F:alpha-glucosidase activity; IEA:EC.
DR
    InterPro; IPR006047; Glyco_hydro_13_cat.
DR
DR
    InterPro; IPR006589; Glyco_hydro_13_sub_cat.
DR
    InterPro; IPR013781; Glyco_hydro_cat.
DR
    Gene3D; G3DSA:3.20.20.80; Glyco hydro cat; 1.
DR
    Pfam; PF00128; Alpha-amylase; 1.
DR
    SMART; SM00642; Aamy; 1.
PΕ
    3: Inferred from homology;
    Complete proteome; Glycosidase; Hydrolase.
ΚW
FT
    CHAIN
               1
                       551
                               Probable alpha-glucosidase.
FT
                                 /FTId=PRO_0000054312.
    ACT_SITE 212
                      212
FT
                                Nucleophile (By similarity).
FT
    ACT_SITE
               272 272
                                Proton donor (By similarity).
    ACT_SITE 345 345
FT
                                By similarity.
    CONFLICT
                13
                       13
                                P \rightarrow A \text{ (in Ref. 1)}.
FT
```

```
CONFLICT
              20
                    21
FT
                           GA \rightarrow RP (in Ref. 1).
FT
    CONFLICT
             402
                   415
                           YGIOFWPDFKGRDG -> MASSSGPTSSAGR (in Ref.
FT
   CONFLICT
FT
             445
                   460
                           PRAVAVQEGDPASVLH -> RGRCRAGGRPGLGAA (in
FT
                           Ref. 1).
            551 AA; 62576 MW; BB7BD3E17C935509 CRC64;
SO
    SEQUENCE
 Query Match
                    54.5%; Score 1595.5; DB 1; Length 551;
 Best Local Similarity 57.3%; Pred. No. 9.7e-113;
 Matches 294; Conservative 74; Mismatches 130; Indels
                                                   15; Gaps
                                                             6;
         3 EWWRGAVTYQVYPRSFQDSNGDGIGDLPGITARLEYLADLGVDAVWLSPFFKSPMKDMGY 62
Qу
           16 DWWRGAVIYQIYPRSFQDTNGDGIGDLQGITARLPHIAGLGADAIWISPFFTSPMRDFGY 75
Db
        63 DVSDYCDVDPVFGTLADFDALLARAHELGLKVIIDQVLSHSSDLHPAFVTSRSDRVNPKA 122
Qу
           Db
        76 DVSNYVDVDPIFGTLEDFDALIAEAHRLGLRVMIDLVLSHTSDRHPWFVESRSSRSNAKA 135
        123 DWYVWADPKPDGSPPNNWLSVFGGSAWAWDARRKOYYLHNFLTSOPDLNYHNPKVODWAL 182
Qу
           136 DWYVWADSKPDGTPPNNWLSIFGGSAWQWDPTRLQYYLHNFLTSQPDLNLHNPQVQEALL 195
Db
        183 DNMRFWLDRGVDGFRFDTVNYFFHDPLLRSNPA---DHRNKPEADG-NPYGMQYHLHDKN 238
Qу
             196 AVERFWLERGVDGFRLDTINFYFHDRELRDNPALVPERRNASTAPAVNPYNYOEHIYDKN 255
Db
        239 QPENLIWMERIRVLLDQYGA-ASVGEMGESHHAIRMMGDYTAPG-RLHQCYSFEFMGYE- 295
Qу
           256 RPENLEFLKRFRAVMDEFPAIAAVGEVGDSQRGLEIAGEYTSGGDKVHMCYAFEFLAPDR 315
Db
        296 YTANLFRDRIESFFKGAPKGWPMWAFSNHDVVRHVSRWAKHGLTPEAVAKOTGALLLSLE 355
QУ
                :| || :||:||
        316 LTPQRVAEVLRDFHRAAPEGWACWAFSNHDVVRHVSRWADGVTDHDAHAKLLASLLMSLR 375
Db
        356 GSICLWEGEELGOTDTELALDELTDPQGIVFWPEPIGRDNTRTPMVWDASPHGGFSTVTP 415
Qу
           376 GTVCIYOGEELALAEAELDYEDLODPYGIOFWPDFKGRDGCRTPMVWESLPDGGFSSATP 435
Db
        416 WLPVKPEOAARHVAGOTGDAASVLESYRAMLAFRRAEPALRTGRTRFLDLAEPVLGFVRG 475
Qу
                   436 WLPISQSHIPRAVAVQEGDPASVLHHYRRFLAFRKANPALAKGEIEFVETRGSLLGFLRS 495
Db
        476 EGEGAILCLFNLS-----PVARGVAVEGVG 500
Qу
              : |||:|
                           1: | :|| |
        496 HGNEKVFCLFNMSDEAATKELPMKRLEPLEGHG 528
```

<!--EndFragment-->